

# Unique identifiers for training materials

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# Learning outcomes

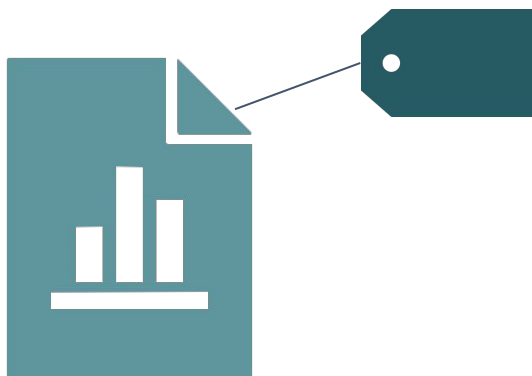
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By the end of this session, you should be able to:

- **Explain** what unique persistent identifiers are and their benefits
- **List** and differentiate the types of unique identifiers that are relevant for publishing and sharing training materials
- **Compare** different strategies for unique identifiers for training materials
- **Create** versioned DOIs for training materials

# What is a unique persistent identifier (PID)

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Identify



Verify



Locate





# Features of PIDs

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- Globally unique
  - It should comply with a **controlled syntax** to avoid clashes
- Persistent
  - It should be **maintained** for a **long period of time**. The syntax used for the identifier should also be persistent
- Resolvable
  - It should allow both **human** and **machine** users to **access the resource**

# Digital Object Identifier - DOI

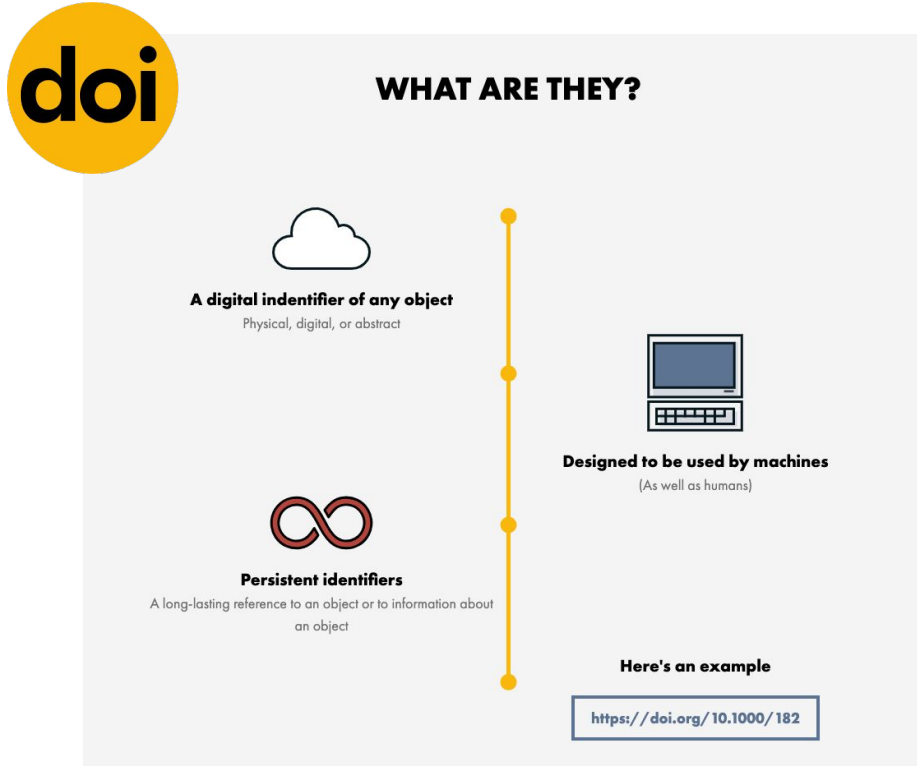


Illustration from the DOI Foundations website  
<https://www.doi.org/the-identifier/what-is-a-doi/>

# Digital Object Identifier - DOI

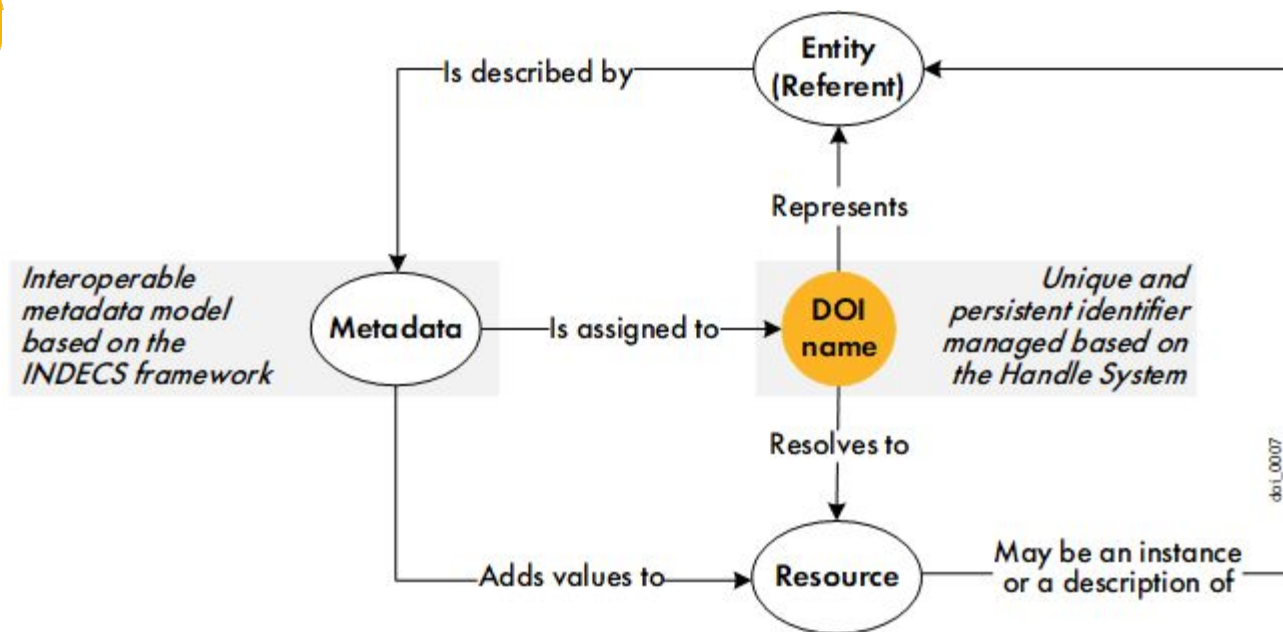


Illustration from The DOI Handbook April 2023 (<https://doi.org/10.1000/182> identifies the latest current version of the handbook)

## Other relevant PIDs



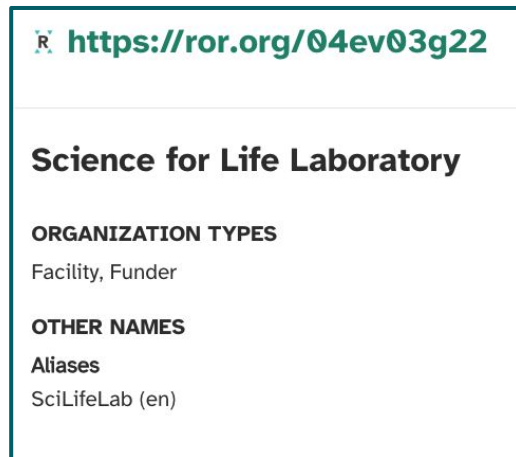
ORCID - Open Researcher and Contributor ID

- persistent identifiers for researchers
- takes homonymy into account
- add aliases to your profile if your name changes
- ORCID stays the same when affiliation changes



The Research Organization Registry

- persistent identifiers for research organizations





# Benefits of PIDs

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- uniquely distinguish resources from similar objects (F)
- a place to keep the metadata (F)
- machine actionable identifiers increase findability (F)
- resolves providing a way or information on how to access the object (A)
- enhances citability leading to easier reuse (R)

# Reflection

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In the context of training materials why are PIDs needed?

Which identifier should be used for each need?

PIDs can help distinguish between:

- different materials - **DOI**
- different versions of the same material - **DOI**
- different authors and contributors - **ORCID**
- different organisations - **ROR**

# Case Study

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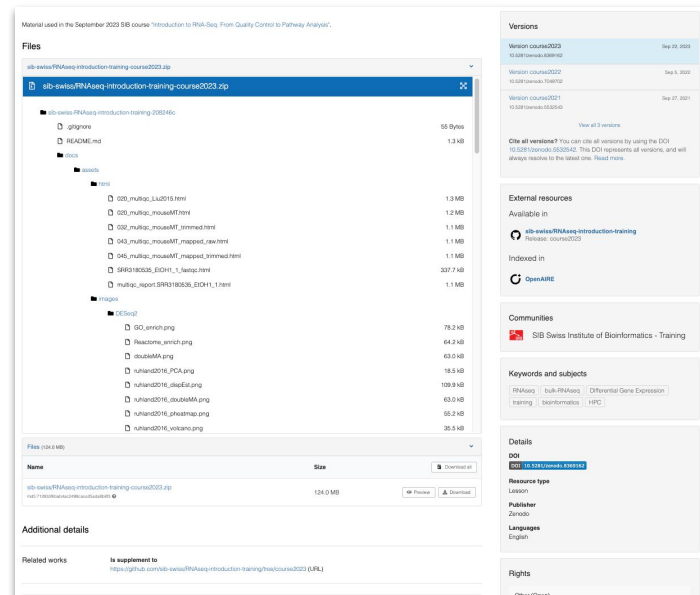
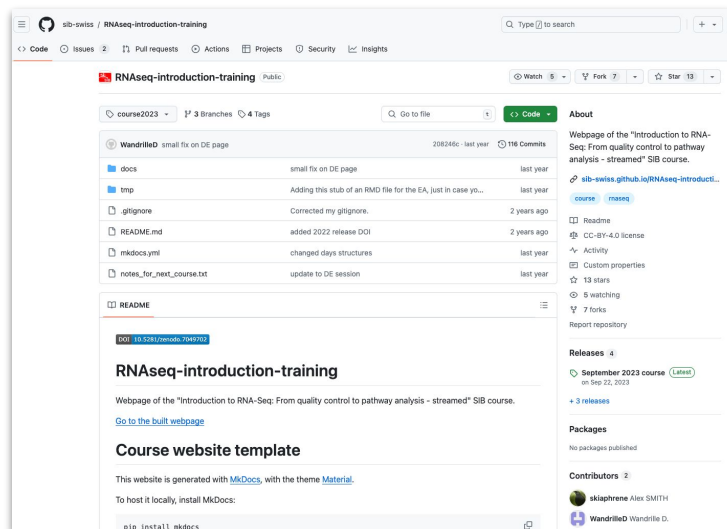
## 1. Group discussion 10 minutes

- a. Assign 1 person to take notes in the shared document
- b. Read through the use case assigned to your group from the FAIR training handbook
- c. Discuss and write down a short summary of the strategy used as well as pros and cons with this strategy

## 2. Plenary discussion 10 minutes

- a. Each group will share their observations and reflections

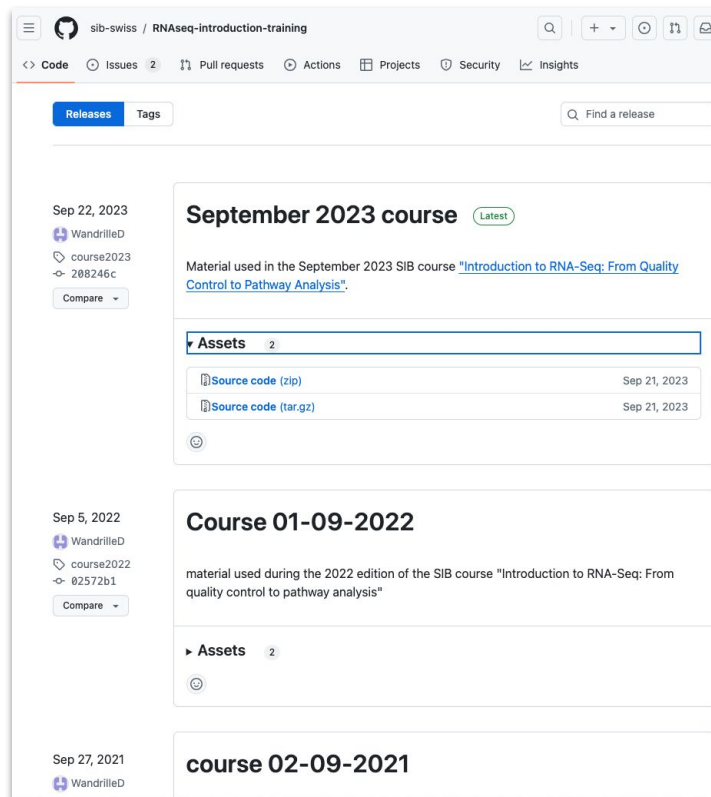
# GitHub integrations



[10.5281/zenodo.5532542](https://doi.org/10.5281/zenodo.5532542)

# GitHub releases

- Snapshot of project at specific time point
- Packaged with re-use in mind
- Downloadable (zip file and tarball)
- Attached with version number/name via a tag
- Release notes to describe the specifics of the snapshot



# Versioned DOIs with releases

Material used in the September 2023 SB course 'Introduction to RNA-Seq: From Quality Control to Pathway Analysis'.

### Files

sb-swissRNAseq-introduction-training-course2023.zip

sb-swissRNAseq-introduction-training-course2023.zip

- sb-swissRNAseq-introduction-training-2023-06
  - gltgloss 55 Bytes
  - README.txt 1.3 kB
  - docs
    - intro
      - 020\_multipart\_L1a2015.html 1.3 MB
      - 020\_multipart\_mouseMT.html 1.2 MB
      - 020\_multipart\_mouseMT\_trimmed.html 1.1 MB
      - 040\_multipart\_mouseMT\_mapped\_raw.html 1.1 MB
      - 040\_multipart\_mouseMT\_mapped\_trimmed.html 1.1 MB
      - SRR185036\_E0H1\_1\_barcode.html 337.7 kB
      - multiple\_report\_SRR185036\_E0H1\_1.html 1.1 MB
    - images
      - GO\_enrichment.png 79.0 kB
      - Reactome\_pathway.png 64.0 kB
      - doubleMA.png 63.0 kB
      - nutan2016\_PCA.png 10.5 kB
      - nutan2016\_dendrogram.png 109.9 kB
      - nutan2016\_doubleMA.png 63.0 kB
      - nutan2016\_gseaheatmap.png 55.2 kB
      - nutan2016\_jockiano.png 35.5 kB

File (10.5 MB)

Name	Size	Download
sb-swissRNAseq-introduction-training-course2023.zip	124.0 MB	Download

Additional details

Related works

It is supplement to  
<https://github.com/sb-swissRNAseq-introduction-training/textcourse2023> (URL)

### Versions

Version	Date
Version course2023	Sep 22, 2023
Version course2022	Sep 5, 2022
Version course2021	Sep 27, 2021

[View all 3 versions](#)

### Cite all versions?

You can cite all versions by using the DOI 10.5281/zenodo.8369162. This DOI represents all versions, and will always resolve to the latest one. [Read more](#).

### External resources

Available in

- [sb-swissRNAseq-introduction-training](#) Release: course2023

Indexed in

- [OpenAIRE](#)

### Communities

[SB Swiss Institute of Bioinformatics - Training](#)

### Keywords and subjects

[Bioinformatics](#) [RNA-Seq](#) [Differential Gene Expression](#) [Training](#) [Information](#) [HTC](#)

### Details

DOI: [10.5281/zenodo.8369162](#)

Resource type: Lesson

Publisher: Zenodo

Languages: English

### Rights

[Other \(Open\)](#)

### Versions

Version course2023	Sep 22, 2023
10.5281/zenodo.8369162	
Version course2022	Sep 5, 2022
10.5281/zenodo.7049702	
Version course2021	Sep 27, 2021
10.5281/zenodo.5532543	

[View all 3 versions](#)

### Cite all versions?

You can cite all versions by using the DOI 10.5281/zenodo.5532542. This DOI represents all versions, and will always resolve to the latest one. [Read more](#).

# Reflection

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How would a good strategy for your own context look like?

Things to consider

- Do you want to get a PID for each training material?
- Do you want to get one PID for your whole training or course?
- Do you want to get a separate PID for each topic/module? For example, for a course containing several topics.
- Do you want to create a collection of topics with a PID where each concept will also have a PID and associated metadata?
- Do you want to get one PID for your whole training or course?

# Introduction to Tutorial

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1. Use  Sandbox to get a DOI for your training material
  - a. By using GitHub integration
  - b. By manually uploading a zip file of your GDrive folder
2. Enrich the Zenodo record with the metadata from previous session
3. Add the DOI to your hosting platform
4. Add the DOI to your TeSS record

Go to the tutorial in [Chapter 08](#)